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Sequence version 5.1.4_456-4578

OM nucleic - nucleic search, using sw model

Run #: March 22, 2003, 21:53:16

(without alignments) (without alignments)

575.5224 Million cell updates/sec

Title: US-03 750 456 393

Perfect score: 484

Sequence: 1...:pr...tt...gg...aa...aa...aa...

Scoring table: IDENTITY_NUC

Gapopen 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8597743376 residues

Total number of hits satisfying chosen parameters: 3498152

Minimum DB seq length: 0

Maximum DB seq length: 2000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : EST:

1: em_estba:*

2: em_esttrum:*

3: em_estinr:*

4: em_estmul:*

5: em_estcv:*

6: em_estfl:*

7: em_estrc:*

8: em_htc:*

9: gb_esti:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_cstom:*

17: gb_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_other:*

25: em_gss_pro:*

26: em_gss_rnd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	467	84.1	838	EM94452
2	195.4	40.4	759	AU07894
3	181.4	37.5	604	BM940073
4	143.8	29	720	AN067452
5	132.8	27.4	448	EP07051
6	122.4	27.1	752	AN067452

EM94452 UI M_EHCP
AU07894 AU07894
BM940073 UI-M_EHCP
AN067452 AN067452
EP07051 EP07051

All:ca@...@mail.nih.gov

Issue Recipient: Dr. James T. M., University of Iowa
CDNA Library Preparation: Dr. M. Bentro Soares, University of Iowa
DNA Sequencing by: Dr. M. Bentro Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be found through the T.M.A.G.E. Consortium at
<http://magelink.nih.gov>
This clone was contributed by the Brain Molecular Anatomy Project (BMAP).

seq flimer: FIX-5
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source

1. 1826

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QY	367	TGTCTGACTGATGGAAAG	330	BG799442/C	RESULT 10
LOCUS		BG799442	551 bp	mRNA	linear EST 21-MAY-2001
DEFINITION		fm9309 5'-Debratish Research Genetics 332 fin Danio rerio cDNA			
Db	382	AATATGCAATGGCGACG	405	mRNA sequence.	
ACCESSION	BG799442				
VERSION	BG799442.1				
KEYWORDS	EST				
SOURCE	zebrafish				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.				
REFERENCE	1 (bases 1 to 551)				
AUTHORS	Clark,M., Johnson,S.L., Lehman,H., Lee,P., Li,F., Marra,M., Brady,J.S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wyllie,T., Underwood,K., Stettler,M., Theising,B., Aller,V., Powers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R., and Wilson,R.				
JOURNAL	WashU-Zebrafish EST Project 1998				
COMMENT	Other ESTs: fm97a09 xl Contact: Stephen L. Johnson Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, Missouri, USA Tel: 314 286 1800 Fax: 314 296 1810 Email: zbrafish@wustl.edu DNA library preparation: Ning Wu, SGN library arrayed by Steve Johnson DNA sequencing by Washington University genome sequencing center Clone distribution: Research Genetics web address: http://www.researchgenetics.com/ Possible reversed clone: similarity on wrong strand High quality sequence stop: 467. Location/Qualifiers				
FEATURES	source				
1. 551 /organism="Danio rerio" /db_xref="taxon:7995" /clone="4468528" /clone lib="Zebrafish Research Genetics 332 fin" /tissue type="fin" /lab host="GeneHogs (HS996, a phage-resistant isolate of DH10B)" /note--"vector: PTTRID-Pac with a modified polylinker; Site_1_EcoRI_Site_2_NotI, 1st strand cDNA was prepared from zebrafish (332) fin, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is non-normalized. Library was constructed by Ning Wu, S.T.E. Others firm this library are only available thru Research Genetics (www.resgen.com/)."					
BASE COUNT	169 a 169 c 155 g 114 t				
ORIGIN					
Query Match	22.5%	Score 108.8, FB 12, Length 551,			
Best Local Similarity	64.0%	Pred. No. 8, 9e-17, Mismatches 89, Indels 0, Gaps 0, Gaps 0			
Matches	158;	Conservative 0, Mismatches 89, Indels 0, Gaps 0, Gaps 0			
QY	229	AGAGCTTGAATGATGGCGACG	297	CY	358 AGGCAACCTCTAATGATGGCGACG
Db	551	AAACGATTCGAACTGGATGAGGTTATGAGGCGATGCGGAGGAT	492	431 AGCTGAGTGAGTACAGCGGCGACGTTGAAAGCTGATGCTGAGC	
DY	298	GTAATGATTTTGTGAGCGATGAACTGGCGTTGCGGCGGCGGCGAGGAG	351	418 TGTATGATGAGTACAGCGGCGACGTTGAAAGCTGATGCTGAGC	
ORIGIN					
Query Match	21.7%	Score 105, FB 17, Length 1054,			
Best Local Similarity	60.2%	Pred. No. 1e-15; Mismatches 207, Conservative 0, Mismatches 133, Indels 4, Gaps 2;			
Matches	207;	Conservative 0, Mismatches 133, Indels 4, Gaps 2;			
QY	14	GAAAGATGAACTGGCGACG	72	DY	199 GGTGAGAGGAGATGTTGATGAGGCGATGCGGAGGATGATGAC
Db	199	GGTGTGAGGAGATGTTGATGAGGCGATGCGGAGGATGATGAC	258		
DY	74	GAAAGATGAACTGGCGACG	133		
RESULT 11					
CREATION	CN30200				
LOCUS	Tetradon nigroviridis	1054 bp	DNA	linear	ggg 12-MAY-2001
DEFINITION	Tetradon nigroviridis genome survey sequence from Tetradon nigroviridis.				
ACCESSION	AL178523				
VERSION	AL178523.1				
KEYWORDS	ggg; genome survey sequence.				
ORGANISM	Tetradon nigroviridis.				
SOURCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Perciformes; Actinopterygii; Percomorphi; Tetraodontiformes; Tetraodontidae; Tetradon				
REFERENCE	1 (bases 1 to 1054)				
AUTHORS	Prost-Crollius,H., Jaijou,C., Pasilva,C., Pizarnik,C., Fisher,C., Bernot,A., Fizames,C., Winckler,P., Bricotier,P., Quetier,F., Saurin,W. and Weissenbach,J.				
JOURNAL	Human gene number estimate provided by genome wide analysis using Tetradon nigroviridis DNA sequence				
REFERENCE	2 (bases 1 to 1054)				
AUTHORS	Poest-Crollius,H., Jaijou,C., Pasilva,C., Pizarnik,C., Fisher,C., Bricotier,P., Rillault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.				
JOURNAL	Submitted (CC-BP-2000)				
COMMENT	This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetradon nigroviridis genome. For more information, please take a look at http://www.genoscope.cnrs.fr/Tetradon .				
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FEATURES	source				
1. 1054 /organism="Tetradon nigroviridis" /db_xref="taxon:9983" /clone="231009" /clone lib="G"					
BASE COUNT	993 a 247 c 247 g 266 t 1 others				
ORIGIN					
Query Match	21.7%	Score 105, FB 17, Length 1054,			
Best Local Similarity	60.2%	Pred. No. 1e-15; Mismatches 207, Conservative 0, Mismatches 133, Indels 4, Gaps 2;			
Matches	207;	Conservative 0, Mismatches 133, Indels 4, Gaps 2;			
QY	14	GAAAGATGAACTGGCGACG	72	DY	199 GGTGAGAGGAGATGTTGATGAGGCGATGCGGAGGATGATGAC
Db	199	GGTGTGAGGAGATGTTGATGAGGCGATGCGGAGGATGATGAC	258		
DY	74	GAAAGATGAACTGGCGACG	133		

